

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: KOSHIBA, TOMOKAZU
- (ii) TITLE OF INVENTION: ALDEHYDE OXIDASE GENE DERIVED FROM PLANT AND UTILIZATION THEREOF
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 - (B) STREET: P.O. BOX 747
 - (C) CITY: FALLS CHURCH
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/943,144
 - (B) FILING DATE: 03-OCT-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: STEWART, RAYMOND C.
 - (B) REGISTRATION NUMBER: 21,066
 - (C) REFERENCE/DOCKET NUMBER: 2185-208P
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (703)205-8000
 - (B) TELEFAX: (703)205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: maize (Zea mays L.)
 - (B) STRAIN: cultivar: Golden Cross Bantam 70

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..4119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCTGTGTT GTGCTGTGCT GCGTGCTGTG GAGGGGGAGG AGGAG ATG GGG AAG	54
Met Gly Lys	
1	
GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC AAC GGC	102
Glu Ala Gly Ala Ala Glu Ser Ser Thr Val Val Leu Ala Val Asn Gly	
5 10 15	
AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG CTG GAG	150
Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser Leu Leu Glu	
20 25 30 35	
TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC TGC GGC	198
Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly	
40 45 50	
GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC GAC CCG	246
Glu Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro	
55 60 65	
GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG ACG CTG	294
Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu	
70 75 80	
CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA ATC GGC	342
Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly	
85 90 95	
AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC GGC TTC	390
Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe	
100 105 110 115	
CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG TCC ATC	438
His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile	
120 125 130	
TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG GAC CCT	486
Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg Pro Asp Pro	
135 140 145	
CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG GCT GTC	534
Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu Lys Ala Val	
150 155 160	
TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT GAC ACC	582
Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Thr	
165 170 175	
TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC CTC AAC	630

- Cys 180	Lys	Ser	Phe	Ala	Ser 185	Asp	Val	Asp	Leu	Glu 190	Asp	Leu	Gly	Leu	Asn 195	
TGT Cys	TTC Phe	TGG Trp	AAG Lys	AAG Lys 200	GGC Gly	GAA Glu	GAA Glu	CCT Pro	GCA Ala 205	GAA Glu	GTC Val	AGC Ser	AGG Arg	CTG Leu 210	CCG Pro	678
GGG Gly	TAC Tyr	AAC Asn	AGC Ser 215	GGT Gly	GCC Ala	GTC Val	TGC Cys	ACC Thr 220	TTT Phe	CCA Pro	GAG Glu	TTT Phe	CTC Leu 225	AAA Lys	TCC Ser	726
GAA Glu	ATC Ile	AAG Lys 230	TCT Ser	ACT Thr	ATG Met	AAG Lys	CAG Gln 235	GTG Val	AAC Asn	GAT Asp	GTC Val	CCC Pro 240	ATT Ile	GCA Ala	GCC Ala	774
TCA Ser	GGT Gly 245	GAT Asp	GGC Gly	TGG Trp	TAC Tyr	CAT His 250	CCT Pro	AAG Lys	AGC Ser	ATT Ile	GAA Glu 255	GAG Glu	CTT Leu	CAC His	AGG Arg	822
TTG Leu 260	TTT Phe	GAT Asp	TCC Ser	AGC Ser	TGG Trp 265	TTT Phe	GAT Asp	GAC Asp	AGT Ser	TCT Ser 270	GTG Val	AAG Lys	ATT Ile	GTT Val	GCT Ala 275	870
TCA Ser	AAC Asn	ACT Thr	GGG Gly 280	TCT Ser	GGA Gly	GTG Val	TAC Tyr	AAG Lys	GAT Asp 285	CAG Gln	GAC Asp	CTC Leu	TAC Tyr	GAC Asp 290	AAG Lys	918
TAC Tyr	ATT Ile	GAC Asp	ATC Ile 295	AAA Lys	GGA Gly	ATC Ile	CCA Pro	GAG Glu 300	CTT Leu	TCA Ser	GTC Val	ATC Ile	AAT Asn 305	AAA Lys	AAC Asn	966
GAC Asp	AAA Lys	GCA Ala 310	ATT Ile	GAG Glu	CTT Leu	GGA Gly 315	TCA Ser	GTT Val	GTG Val	TCC Ser	ATC Ile	TCT Ser 320	AAA Lys	GCT Ala	ATT Ile	1014
GAA Glu 325	GTG Val	CTG Leu	TCA Ser	GAT Asp	GGA Gly	AAT Asn 330	TTG Leu	GTC Val	TTC Phe	AGA Arg	AAG Lys 335	ATT Ile	GCT Ala	GAT Asp	CAC His	1062
CTC Leu 340	AAC Asn	AAA Lys	GTG Val	GCT Ala	TCA Ser 345	CCG Pro	TTT Phe	GTT Val	CGG Arg	AAC Asn 350	ACT Thr	GCA Ala	ACC Thr	ATA Ile	GGA Gly 355	1110
GGA Gly	AAC Asn	ATA Ile	ATG Met 360	ATG Met	GCA Ala	CAA Gln	AGG Arg	TTG Leu	CCA Pro 365	TTT Phe	GAA Glu	TCG Ser	GAT Asp	GTT Val 370	GCA Ala	1158
ACC Thr	GTG Val	CTC Leu	CTA Leu 375	GCT Ala	GCG Ala	GGT Gly	TCG Ser	ACA Thr 380	GTC Val	ACA Thr	GTC Val	CAG Gln	GTG Val 385	GCT Ala	TCC Ser	1206
AAA Lys	AGG Arg	CTG Leu 390	TGC Cys	TTC Phe	ACT Thr	CTG Leu 395	GAG Glu 395	GAA Glu	TTC Phe	TTG Leu	GAA Glu	CAA Gln 400	CCT Pro	CCA Pro	TGT Cys	1254
GAT	TCT	AGG	ACC	CTG	CTG	CTG	AGC	ATA	TTT	ATC	CCA	GAA	TGG	GGT	TCA	1302

-Asp	Ser	Arg	Thr	Leu	Leu	Leu	Ser	Ile	Phe	Ile	Pro	Glu	Trp	Gly	Ser	
	405					410					415					
GAC	TAT	GTC	ACC	TTT	GAG	ACT	TTC	CGA	GCC	GCC	CCA	CGA	CCA	TTT	GGA	1350
Asp	Tyr	Val	Thr	Phe	Glu	Thr	Phe	Arg	Ala	Ala	Pro	Arg	Pro	Phe	Gly	
420					425					430					435	
AAT	GCT	GTC	TCT	TAT	GTA	AAC	TCT	GCT	TTC	TTG	GCA	AGG	ACA	TCA	GGC	1398
Asn	Ala	Val	Ser	Tyr	Val	Asn	Ser	Ala	Phe	Leu	Ala	Arg	Thr	Ser	Gly	
				440					445					450		
AGC	CTT	CTA	ATT	GAG	GAT	ATA	TGC	TTG	GCA	TTT	GGT	GCC	TAC	GGA	GTC	1446
Ser	Leu	Leu	Ile	Glu	Asp	Ile	Cys	Leu	Ala	Phe	Gly	Ala	Tyr	Gly	Val	
			455					460					465			
GAT	CAT	GCC	ATC	AGA	GCT	AAG	AAG	GTT	GAA	GAT	TTC	TTG	AAG	GGA	AAA	1494
Asp	His	Ala	Ile	Arg	Ala	Lys	Lys	Val	Glu	Asp	Phe	Leu	Lys	Gly	Lys	
		470					475					480				
TCG	CTG	AGC	TCA	TTT	GTG	ATA	CTT	GAA	GCA	ATT	AAA	CTA	CTC	AAA	GAT	1542
Ser	Leu	Ser	Ser	Phe	Val	Ile	Leu	Glu	Ala	Ile	Lys	Leu	Leu	Lys	Asp	
	485					490					495					
ACC	GTT	TCA	CCA	TCA	GAA	GGC	ACT	ACA	CAT	CAT	GAA	TAC	AGG	GTC	AGC	1590
Thr	Val	Ser	Pro	Ser	Glu	Gly	Thr	Thr	His	His	Glu	Tyr	Arg	Val	Ser	
500					505					510					515	
TTG	GCT	GTC	AGT	TTC	TTG	TTC	AGT	TTC	TTA	TCT	TCC	CTT	GCC	AAC	AGT	1638
Leu	Ala	Val	Ser	Phe	Leu	Phe	Ser	Phe	Leu	Ser	Ser	Leu	Ala	Asn	Ser	
				520				525						530		
TCG	AGT	GCA	CCA	TCA	AAT	ATT	GAT	ACT	CCC	AAT	GGG	TCA	TAT	ACT	CAT	1686
Ser	Ser	Ala	Pro	Ser	Asn	Ile	Asp	Thr	Pro	Asn	Gly	Ser	Tyr	Thr	His	
			535				540						545			
GAA	ACT	GGT	AGC	AAT	GTG	GAC	TCA	CCT	GAG	AGG	CAT	ATT	AAG	GTT	GAC	1734
Glu	Thr	Gly	Ser	Asn	Val	Asp	Ser	Pro	Glu	Arg	His	Ile	Lys	Val	Asp	
		550				555						560				
AGC	AAT	GAT	TTG	CCA	ATT	CGT	TCA	AGA	CAA	GAA	ATG	GTT	TTT	AGC	GAT	1782
Ser	Asn	Asp	Leu	Pro	Ile	Arg	Ser	Arg	Gln	Glu	Met	Val	Phe	Ser	Asp	
	565					570					575					
GAG	TAC	AAG	CCT	GTT	GGC	AAG	CCG	ATC	AAG	AAA	GTC	GGG	GCA	GAG	ATC	1830
Glu	Tyr	Lys	Pro	Val	Gly	Lys	Pro	Ile	Lys	Lys	Val	Gly	Ala	Glu	Ile	
580					585					590					595	
CAA	GCA	TCA	GGG	GAG	GCT	GTG	TAC	GTT	GAT	GAT	ATC	CCT	GCT	CCC	AAG	1878
Gln	Ala	Ser	Gly	Glu	Ala	Val	Tyr	Val	Asp	Asp	Ile	Pro	Ala	Pro	Lys	
			600						605					610		
GAT	TGC	CTC	TAT	GGA	GCA	TTT	ATC	TAC	AGC	ACA	CAT	CCT	CAT	GCT	CAT	1926
Asp	Cys	Leu	Tyr	Gly	Ala	Phe	Ile	Tyr	Ser	Thr	His	Pro	His	Ala	His	
			615					620					625			
GTG	AGA	AGT	ATC	AAC	TTC	AAA	TCA	TCC	TTG	GCT	TCA	CAG	AAG	GTC	ATC	1974

Val	Arg	Ser 630	Ile	Asn	Phe	Lys	Ser 635	Ser	Leu	Ala	Ser	Gln 640	Lys	Val	Ile	
ACA Thr	GTT Val	ATA Ile	ACC Thr	GCA Ala	AAG Lys	GAT Asp	ATT Ile	CCA Pro	AGC Ser	GGT Gly	GGA Gly	GAA Glu	AAT Asn	ATT Ile	GGA Gly	2022
AGC Ser	AGC Ser	TTC Phe	CTG Leu	ATG Met	CAA Gln	GGA Gly	GAA Glu	GCA Ala	CTA Leu	TTT Phe	GCA Ala	GAT Asp	CCA Pro	ATC Ile	GCT Ala	2070
GAA Glu	TTT Phe	GCT Ala	GGT Gly	CAA Gln	AAT Asn	ATT Ile	GGT Gly	GTC Val	GTG Val	ATT Ile	GCT Ala	GAA Glu	ACA Thr	CAA Gln	AGA Arg	2118
TAT Tyr	GCT Ala	AAT Asn	ATG Met	GCT Ala	GCA Ala	AAG Lys	CAA Gln	GCT Ala	GTT Val	GTT Val	GAG Glu	TAT Tyr	AGC Ser	ACA Thr	GAA Glu	2166
AAT Asn	CTG Leu	CAG Gln	CCA Pro	CCA Pro	ATT Ile	CTG Leu	ACA Thr	ATA Ile	GAA Glu	GAT Asp	GCC Ala	ATC Ile	CAA Gln	AGA Arg	AAC Asn	2214
AGC Ser	TAC Tyr	ATC Ile	CAA Gln	ATT Ile	CCC Pro	CCA Pro	TTT Phe	TTA Leu	GCT Ala	CCA Pro	AAG Lys	CCA Pro	GTT Val	GGT Gly	GAC Asp	2262
TAC Tyr	AAC Asn	AAA Lys	GGG Gly	ATG Met	GCT Ala	GAA Glu	GCA Ala	GAC Asp	CAC His	AAG Lys	ATT Ile	CTA Leu	TCA Ser	GCA Ala	GAG Glu	2310
GTA Val	AAA Lys	CTT Leu	GAA Glu	TCC Ser	CAG Gln	TAC Tyr	TAC Tyr	TTC Phe	TAC Tyr	ATG Met	GAA Glu	ACT Thr	CAA Gln	GCA Ala	GCA Ala	2358
CTA Leu	GCG Ala	ATT Ile	CCT Pro	GAT Asp	GAA Glu	GAT Asp	AAC Asn	TGC Cys	ATA Ile	ACA Thr	ATC Ile	TAT Tyr	TCC Ser	TCG Ser	ACA Thr	2406
CAA Gln	ATG Met	CCT Pro	GAG Glu	CTC Leu	ACA Thr	CAA Gln	AAT Asn	TTG Leu	ATA Ile	GCA Ala	AGG Arg	TGT Cys	CTT Leu	GGC Gly	ATT Ile	2454
CCA Pro	TTT Phe	CAC His	AAT Asn	GTC Val	CGT Arg	GTC Val	ATC Ile	AGC Ser	AGA Arg	AGA Arg	GTA Val	GGA Gly	GGA Gly	GGC Gly	TTT Phe	2502
GGT Gly	GGA Gly	AAG Lys	GCA Ala	ATG Met	AAA Lys	GCA Ala	ACG Thr	CAT His	ACT Thr	GCA Ala	TGT Cys	GCA Ala	TGT Cys	GCC Ala	CTT Leu	2550
GCT Ala	GCC Ala	TTC Phe	AAG Lys	CTG Leu	CGG Arg	CGT Arg	CCA Pro	GTT Val	AGG Arg	ATG Met	TAC Tyr	CTC Leu	GAT Asp	CGC Arg	AAG Lys	2598
ACG	GAC	ATG	ATA	ATG	GCT	GGA	GGG	AGA	CAT	CCA	ATG	AAG	GCG	AAG	TAC	2646

Thr	Asp	Met	Ile	Met	Ala	Gly	Gly	Arg	His	Pro	Met	Lys	Ala	Lys	Tyr	
			855					860					865			
TCT	GTT	GGG	TTC	AAG	TCA	GAT	GGC	AAG	ATC	ACA	GCC	TTG	CAC	CTA	GAT	2694
Ser	Val	Gly	Phe	Lys	Ser	Asp	Gly	Lys	Ile	Thr	Ala	Leu	His	Leu	Asp	
		870					875					880				
CTT	GGA	ATC	AAT	GCT	GGA	ATA	TCA	CCA	GAT	GTG	AGT	CCA	TTG	ATG	CCA	2742
Leu	Gly	Ile	Asn	Ala	Gly	Ile	Ser	Pro	Asp	Val	Ser	Pro	Leu	Met	Pro	
	885					890					895					
CGT	GCT	ATC	ATA	GGA	GCT	CTC	AAA	AAG	TAC	AAC	TGG	GGC	ACT	CTT	GAA	2790
Arg	Ala	Ile	Ile	Gly	Ala	Leu	Lys	Lys	Tyr	Asn	Trp	Gly	Thr	Leu	Glu	
900					905					910					915	
TTT	GAC	ACC	AAG	GTC	TGC	AAG	ACA	AAT	GTC	TCA	TCA	AAG	TCA	GCA	ATG	2838
Phe	Asp	Thr	Lys	Val	Cys	Lys	Thr	Asn	Val	Ser	Ser	Lys	Ser	Ala	Met	
				920					925					930		
CGA	GCT	CCT	GGA	GAT	GTG	CAG	GGC	TCT	TTC	ATC	GCT	GAA	GCC	ATC	ATC	2886
Arg	Ala	Pro	Gly	Asp	Val	Gln	Gly	Ser	Phe	Ile	Ala	Glu	Ala	Ile	Ile	
			935					940					945			
GAG	CAT	GTT	GCC	TCA	GCA	CTC	GCA	CTA	GAC	ACT	AAC	ACC	GTC	AGG	AGG	2934
Glu	His	Val	Ala	Ser	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Thr	Val	Arg	Arg	
		950					955					960				
AAG	AAC	CTT	CAT	GAT	TTT	GAA	AGC	CTT	GAA	GTT	TTC	TAT	GGA	GAA	AGT	2982
Lys	Asn	Leu	His	Asp	Phe	Glu	Ser	Leu	Glu	Val	Phe	Tyr	Gly	Glu	Ser	
	965					970					975					
GCA	GGT	GAA	GCT	TCT	ACA	TAC	AGC	CTG	GTT	TCC	ATG	TTT	GAC	AAG	CTG	3030
Ala	Gly	Glu	Ala	Ser	Thr	Tyr	Ser	Leu	Val	Ser	Met	Phe	Asp	Lys	Leu	
980					985				990						995	
GCC	TTG	TCT	CCA	GAA	TAC	CAG	CAC	AGG	GCT	GCA	ATG	ATT	GAG	CAG	TTC	3078
Ala	Leu	Ser	Pro	Glu	Tyr	Gln	His	Arg	Ala	Ala	Met	Ile	Glu	Gln	Phe	
			1000						1005					1010		
AAT	AGC	AGC	AAC	AAA	TGG	AAG	AAA	CGC	GGC	ATT	TCT	TGT	GTG	CCA	GCC	3126
Asn	Ser	Ser	Asn	Lys	Trp	Lys	Lys	Arg	Gly	Ile	Ser	Cys	Val	Pro	Ala	
			1015					1020					1025			
ACT	TAT	GAG	GTT	AAT	CTT	CGA	CCA	ACT	CCA	GGC	AAG	GTG	TCA	ATC	ATG	3174
Thr	Tyr	Glu	Val	Asn	Leu	Arg	Pro	Thr	Pro	Gly	Lys	Val	Ser	Ile	Met	
		1030					1035					1040				
AAT	GAT	GGT	TCC	ATC	GCT	GTC	GAG	GTT	GGA	GGA	ATT	GAG	ATA	GGT	CAA	3222
Asn	Asp	Gly	Ser	Ile	Ala	Val	Glu	Val	Gly	Gly	Ile	Glu	Ile	Gly	Gln	
	1045					1050					1055					
GGA	TTG	TGG	ACT	AAA	GTG	AAG	CAG	ATG	ACG	GCC	TTT	GGA	CTG	GGA	CAG	3270
Gly	Leu	Trp	Thr	Lys	Val	Lys	Gln	Met	Thr	Ala	Phe	Gly	Leu	Gly	Gln	
1060					1065					1070					1075	
CTG	TGT	CCT	GAT	GGT	GGC	GAA	TGC	CTT	CTG	GAC	AAG	GTT	CGG	GTT	ATC	3318

-Leu	Cys	Pro	Asp	Gly	Gly	Glu	Cys	Leu	Leu	Asp	Lys	Val	Arg	Val	Ile	
				1080					1085					1090		
CAG	GCA	GAC	ACA	TTA	AGC	CTG	ATC	CAA	GGA	GGT	ATG	ACT	GCT	GGG	AGC	3366
Gln	Ala	Asp	Thr	Leu	Ser	Leu	Ile	Gln	Gly	Gly	Met	Thr	Ala	Gly	Ser	
			1095					1100					1105			
ACC	ACT	TCT	GAA	ACT	AGC	TGT	GAA	ACA	GTT	CGG	CAA	TCT	TGT	GTT	GCA	3414
Thr	Thr	Ser	Glu	Thr	Ser	Cys	Glu	Thr	Val	Arg	Gln	Ser	Cys	Val	Ala	
		1110					1115					1120				
CTG	GTT	GAG	AAG	CTG	AAC	CCT	ATC	AAG	GAG	AGT	CTC	GAA	GCT	AAG	TCC	3462
Leu	Val	Glu	Lys	Leu	Asn	Pro	Ile	Lys	Glu	Ser	Leu	Glu	Ala	Lys	Ser	
	1125					1130					1135					
AAC	ACA	GTG	GAA	TGG	AGT	GCC	TTG	ATT	GCT	CAG	GCA	AGC	ATG	GCG	AGT	3510
Asn	Thr	Val	Glu	Trp	Ser	Ala	Leu	Ile	Ala	Gln	Ala	Ser	Met	Ala	Ser	
1140					1145					1150					1155	
GTG	AAC	CTA	TCA	GCA	CAG	CCG	TAC	TGG	ACT	CCT	GAT	CCA	TCT	TTC	AAG	3558
Val	Asn	Leu	Ser	Ala	Gln	Pro	Tyr	Trp	Thr	Pro	Asp	Pro	Ser	Phe	Lys	
				1160					1165					1170		
AGC	TAC	TTG	AAC	TAC	GGA	GCT	GGC	ACC	AGT	GAG	GTG	GAA	GTT	GAT	ATC	3606
Ser	Tyr	Leu	Asn	Tyr	Gly	Ala	Gly	Thr	Ser	Glu	Val	Glu	Val	Asp	Ile	
			1175					1180					1185			
CTA	ACA	GGA	GCA	ACC	ACA	ATT	CTG	CGA	AGC	GAC	CTG	GTG	TAT	GAC	TGC	3654
Leu	Thr	Gly	Ala	Thr	Thr	Ile	Leu	Arg	Ser	Asp	Leu	Val	Tyr	Asp	Cys	
		1190					1195					1200				
GGG	CAG	AGC	CTA	AAC	CCT	GCT	GTA	GAC	TTG	GGC	CAG	ATC	GAG	GGC	TGC	3702
Gly	Gln	Ser	Leu	Asn	Pro	Ala	Val	Asp	Leu	Gly	Gln	Ile	Glu	Gly	Cys	
	1205					1210					1215					
TTT	GTC	CAA	GGA	ATA	GGG	TTC	TTC	ACG	AAC	GAG	GAC	TAC	AAG	ACG	AAT	3750
Phe	Val	Gln	Gly	Ile	Gly	Phe	Phe	Thr	Asn	Glu	Asp	Tyr	Lys	Thr	Asn	
1220				1225						1230					1235	
TCC	GAC	GGG	TTG	GTC	ATC	CAC	GAC	GGC	ACA	TGG	ACG	TAC	AAG	ATC	CCC	3798
Ser	Asp	Gly	Leu	Val	Ile	His	Asp	Gly	Thr	Trp	Thr	Tyr	Lys	Ile	Pro	
				1240				1245						1250		
ACG	GTG	GAT	AAT	ATC	CCG	AAG	GAG	TTC	AAT	GTT	GAG	ATG	TTT	AAC	AGC	3846
Thr	Val	Asp	Asn	Ile	Pro	Lys	Glu	Phe	Asn	Val	Glu	Met	Phe	Asn	Ser	
			1255				1260						1265			
GCC	CCT	GAC	AAG	AAG	CGT	GTC	CTA	TCT	TCC	AAA	GCG	TCG	GGC	GAG	CCG	3894
Ala	Pro	Asp	Lys	Lys	Arg	Val	Leu	Ser	Ser	Lys	Ala	Ser	Gly	Glu	Pro	
		1270					1275					1280				
CCG	CTG	GTT	CTC	GCA	ACC	TCG	GTG	CAC	TGC	GCG	ATG	AGG	GAG	GCC	ATC	3942
Pro	Leu	Val	Leu	Ala	Thr	Ser	Val	His	Cys	Ala	Met	Arg	Glu	Ala	Ile	
	1285					1290				1295						
AGG	GCG	GCG	AGG	AAG	GAG	TTC	TCG	GTC	AGC	ACC	AGC	CCC	GCG	AAA	TCC	3990

Arg	Ala	Ala	Arg	Lys	Glu	Phe	Ser	Val	Ser	Thr	Ser	Pro	Ala	Lys	Ser	
1300					1305					1310					1315	
GCC	GTC	ACA	TTC	CAG	ATG	GAC	GTG	CCG	GCG	ACG	ATG	CCT	GTC	GTC	AAG	4038
Ala	Val	Thr	Phe	Gln	Met	Asp	Val	Pro	Ala	Thr	Met	Pro	Val	Val	Lys	
				1320					1325					1330		
GAG	CTC	TGC	GGC	CTC	GAC	GTC	GTG	GAG	AGG	TAC	CTC	GAG	AAC	GTG	TCT	4086
Glu	Leu	Cys	Gly	Leu	Asp	Val	Val	Glu	Arg	Tyr	Leu	Glu	Asn	Val	Ser	
			1335					1340					1345			
GCC	GCC	AGT	GCC	GGC	CCA	AAC	ACA	GCG	AAA	GCA	TAGATCCAGC	AGGCCTCAGG				4139
Ala	Ala	Ser	Ala	Gly	Pro	Asn	Thr	Ala	Lys	Ala						
			1350					1355								
GTGCAGTCCG	CGCACTGCCA	GAGATGATGT	GTGCTGCCCT	GATGTACAGA	CAGTACAGTA											4199
CAGAGGAGAG	AGAATTGGGG	GAAGTCAGGA	ACTGCGAGGA	GCGATGAACA	GTATATAGAG											4259
TGAAAAATAA	AAGTGCTTCG	TACTAATAAT	CACTAGAAAA	AATTATGCAC	ATCTCCCACG											4319
CACTACCGGC	ACGACTGTTG	AATATTTTGT	AAAATAAGAT	GTCATAAGCT	ATTTATTTTC											4379
TGTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA													4412

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1358 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Lys	Glu	Ala	Gly	Ala	Ala	Glu	Ser	Ser	Thr	Val	Val	Leu	Ala	
1				5				10						15		
Val	Asn	Gly	Lys	Arg	Tyr	Glu	Ala	Ala	Gly	Val	Ala	Pro	Ser	Thr	Ser	
			20				25					30				
Leu	Leu	Glu	Phe	Leu	Arg	Thr	Gln	Thr	Pro	Val	Arg	Gly	Pro	Lys	Leu	
		35				40					45					
Gly	Cys	Gly	Glu	Gly	Gly	Cys	Gly	Ala	Cys	Val	Val	Leu	Val	Ser	Lys	
	50					55					60					
Tyr	Asp	Pro	Ala	Thr	Asp	Glu	Val	Thr	Glu	Phe	Ser	Ala	Ser	Ser	Cys	
65				70					75						80	
Leu	Thr	Leu	Leu	His	Ser	Val	Asp	Arg	Cys	Ser	Val	Thr	Thr	Ser	Glu	
			85					90						95		
Gly	Ile	Gly	Asn	Thr	Arg	Asp	Gly	Tyr	His	Pro	Val	Gln	Gln	Arg	Leu	

100						105						110					
Ser	Gly	Phe	His	Ala	Ser	Gln	Cys	Gly	Phe	Cys	Thr	Pro	Gly	Met	Cys		
		115					120					125					
Met	Ser	Ile	Phe	Ser	Ala	Leu	Val	Lys	Ala	Asp	Asn	Lys	Ser	Asp	Arg		
	130					135					140						
Pro	Asp	Pro	Pro	Ala	Gly	Phe	Ser	Lys	Ile	Thr	Thr	Ser	Glu	Ala	Glu		
145					150					155					160		
Lys	Ala	Val	Ser	Gly	Asn	Leu	Cys	Arg	Cys	Thr	Gly	Tyr	Arg	Pro	Ile		
				165					170					175			
Val	Asp	Thr	Cys	Lys	Ser	Phe	Ala	Ser	Asp	Val	Asp	Leu	Glu	Asp	Leu		
			180					185					190				
Gly	Leu	Asn	Cys	Phe	Trp	Lys	Lys	Gly	Glu	Glu	Pro	Ala	Glu	Val	Ser		
		195					200					205					
Arg	Leu	Pro	Gly	Tyr	Asn	Ser	Gly	Ala	Val	Cys	Thr	Phe	Pro	Glu	Phe		
	210					215					220						
Leu	Lys	Ser	Glu	Ile	Lys	Ser	Thr	Met	Lys	Gln	Val	Asn	Asp	Val	Pro		
225					230					235					240		
Ile	Ala	Ala	Ser	Gly	Asp	Gly	Trp	Tyr	His	Pro	Lys	Ser	Ile	Glu	Glu		
				245					250					255			
Leu	His	Arg	Leu	Phe	Asp	Ser	Ser	Trp	Phe	Asp	Asp	Ser	Ser	Val	Lys		
			260					265					270				
Ile	Val	Ala	Ser	Asn	Thr	Gly	Ser	Gly	Val	Tyr	Lys	Asp	Gln	Asp	Leu		
		275					280					285					
Tyr	Asp	Lys	Tyr	Ile	Asp	Ile	Lys	Gly	Ile	Pro	Glu	Leu	Ser	Val	Ile		
	290					295					300						
Asn	Lys	Asn	Asp	Lys	Ala	Ile	Glu	Leu	Gly	Ser	Val	Val	Ser	Ile	Ser		
305					310					315					320		
Lys	Ala	Ile	Glu	Val	Leu	Ser	Asp	Gly	Asn	Leu	Val	Phe	Arg	Lys	Ile		
				325					330					335			
Ala	Asp	His	Leu	Asn	Lys	Val	Ala	Ser	Pro	Phe	Val	Arg	Asn	Thr	Ala		
			340					345					350				
Thr	Ile	Gly	Gly	Asn	Ile	Met	Met	Ala	Gln	Arg	Leu	Pro	Phe	Glu	Ser		
		355					360						365				
Asp	Val	Ala	Thr	Val	Leu	Leu	Ala	Ala	Gly	Ser	Thr	Val	Thr	Val	Gln		
	370					375					380						
Val	Ala	Ser	Lys	Arg	Leu	Cys	Phe	Thr	Leu	Glu	Glu	Phe	Leu	Glu	Gln		
385					390					395					400		

-Pro	Pro	Cys	Asp	Ser	Arg	Thr	Leu	Leu	Leu	Ser	Ile	Phe	Ile	Pro	Glu	405	410	415
Trp	Gly	Ser	Asp	Tyr	Val	Thr	Phe	Glu	Thr	Phe	Arg	Ala	Ala	Pro	Arg	420	425	430
Pro	Phe	Gly	Asn	Ala	Val	Ser	Tyr	Val	Asn	Ser	Ala	Phe	Leu	Ala	Arg	435	440	445
Thr	Ser	Gly	Ser	Leu	Leu	Ile	Glu	Asp	Ile	Cys	Leu	Ala	Phe	Gly	Ala	450	455	460
Tyr	Gly	Val	Asp	His	Ala	Ile	Arg	Ala	Lys	Lys	Val	Glu	Asp	Phe	Leu	465	470	475
Lys	Gly	Lys	Ser	Leu	Ser	Ser	Phe	Val	Ile	Leu	Glu	Ala	Ile	Lys	Leu	485	490	495
Leu	Lys	Asp	Thr	Val	Ser	Pro	Ser	Glu	Gly	Thr	Thr	His	His	Glu	Tyr	500	505	510
Arg	Val	Ser	Leu	Ala	Val	Ser	Phe	Leu	Phe	Ser	Phe	Leu	Ser	Ser	Leu	515	520	525
Ala	Asn	Ser	Ser	Ser	Ala	Pro	Ser	Asn	Ile	Asp	Thr	Pro	Asn	Gly	Ser	530	535	540
Tyr	Thr	His	Glu	Thr	Gly	Ser	Asn	Val	Asp	Ser	Pro	Glu	Arg	His	Ile	545	550	555
Lys	Val	Asp	Ser	Asn	Asp	Leu	Pro	Ile	Arg	Ser	Arg	Gln	Glu	Met	Val	565	570	575
Phe	Ser	Asp	Glu	Tyr	Lys	Pro	Val	Gly	Lys	Pro	Ile	Lys	Lys	Val	Gly	580	585	590
Ala	Glu	Ile	Gln	Ala	Ser	Gly	Glu	Ala	Val	Tyr	Val	Asp	Asp	Ile	Pro	595	600	605
Ala	Pro	Lys	Asp	Cys	Leu	Tyr	Gly	Ala	Phe	Ile	Tyr	Ser	Thr	His	Pro	610	615	620
His	Ala	His	Val	Arg	Ser	Ile	Asn	Phe	Lys	Ser	Ser	Leu	Ala	Ser	Gln	625	630	635
Lys	Val	Ile	Thr	Val	Ile	Thr	Ala	Lys	Asp	Ile	Pro	Ser	Gly	Gly	Glu	645	650	655
Asn	Ile	Gly	Ser	Ser	Phe	Leu	Met	Gln	Gly	Glu	Ala	Leu	Phe	Ala	Asp	660	665	670
Pro	Ile	Ala	Glu	Phe	Ala	Gly	Gln	Asn	Ile	Gly	Val	Val	Ile	Ala	Glu	675	680	685
Thr	Gln	Arg	Tyr	Ala	Asn	Met	Ala	Ala	Lys	Gln	Ala	Val	Val	Glu	Tyr	690	695	700

Ser	Thr	Glu	Asn	Leu	Gln	Pro	Pro	Ile	Leu	Thr	Ile	Glu	Asp	Ala	Ile	705	710	715	720
Gln	Arg	Asn	Ser	Tyr	Ile	Gln	Ile	Pro	Pro	Phe	Leu	Ala	Pro	Lys	Pro		725	730	735
Val	Gly	Asp	Tyr	Asn	Lys	Gly	Met	Ala	Glu	Ala	Asp	His	Lys	Ile	Leu		740	745	750
Ser	Ala	Glu	Val	Lys	Leu	Glu	Ser	Gln	Tyr	Tyr	Phe	Tyr	Met	Glu	Thr		755	760	765
Gln	Ala	Ala	Leu	Ala	Ile	Pro	Asp	Glu	Asp	Asn	Cys	Ile	Thr	Ile	Tyr		770	775	780
Ser	Ser	Thr	Gln	Met	Pro	Glu	Leu	Thr	Gln	Asn	Leu	Ile	Ala	Arg	Cys		785	790	800
Leu	Gly	Ile	Pro	Phe	His	Asn	Val	Arg	Val	Ile	Ser	Arg	Arg	Val	Gly		805	810	815
Gly	Gly	Phe	Gly	Gly	Lys	Ala	Met	Lys	Ala	Thr	His	Thr	Ala	Cys	Ala		820	825	830
Cys	Ala	Leu	Ala	Ala	Phe	Lys	Leu	Arg	Arg	Pro	Val	Arg	Met	Tyr	Leu		835	840	845
Asp	Arg	Lys	Thr	Asp	Met	Ile	Met	Ala	Gly	Gly	Arg	His	Pro	Met	Lys		850	855	860
Ala	Lys	Tyr	Ser	Val	Gly	Phe	Lys	Ser	Asp	Gly	Lys	Ile	Thr	Ala	Leu		865	870	875
His	Leu	Asp	Leu	Gly	Ile	Asn	Ala	Gly	Ile	Ser	Pro	Asp	Val	Ser	Pro		885	890	895
Leu	Met	Pro	Arg	Ala	Ile	Ile	Gly	Ala	Leu	Lys	Lys	Tyr	Asn	Trp	Gly		900	905	910
Thr	Leu	Glu	Phe	Asp	Thr	Lys	Val	Cys	Lys	Thr	Asn	Val	Ser	Ser	Lys		915	920	925
Ser	Ala	Met	Arg	Ala	Pro	Gly	Asp	Val	Gln	Gly	Ser	Phe	Ile	Ala	Glu		930	935	940
Ala	Ile	Ile	Glu	His	Val	Ala	Ser	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Thr		945	950	955
Val	Arg	Arg	Lys	Asn	Leu	His	Asp	Phe	Glu	Ser	Leu	Glu	Val	Phe	Tyr		965	970	975
Gly	Glu	Ser	Ala	Gly	Glu	Ala	Ser	Thr	Tyr	Ser	Leu	Val	Ser	Met	Phe		980	985	990
Asp	Lys	Leu	Ala	Leu	Ser	Pro	Glu	Tyr	Gln	His	Arg	Ala	Ala	Met	Ile		995	1000	1005

-Glu	Gln	Phe	Asn	Ser	Ser	Asn	Lys	Trp	Lys	Lys	Arg	Gly	Ile	Ser	Cys	
1010						1015					1020					
Val	Pro	Ala	Thr	Tyr	Glu	Val	Asn	Leu	Arg	Pro	Thr	Pro	Gly	Lys	Val	
1025					1030					1035					1040	
Ser	Ile	Met	Asn	Asp	Gly	Ser	Ile	Ala	Val	Glu	Val	Gly	Gly	Ile	Glu	
			1045						1050					1055		
Ile	Gly	Gln	Gly	Leu	Trp	Thr	Lys	Val	Lys	Gln	Met	Thr	Ala	Phe	Gly	
			1060					1065					1070			
Leu	Gly	Gln	Leu	Cys	Pro	Asp	Gly	Gly	Glu	Cys	Leu	Leu	Asp	Lys	Val	
		1075					1080					1085				
Arg	Val	Ile	Gln	Ala	Asp	Thr	Leu	Ser	Leu	Ile	Gln	Gly	Gly	Met	Thr	
1090						1095					1100					
Ala	Gly	Ser	Thr	Thr	Ser	Glu	Thr	Ser	Cys	Glu	Thr	Val	Arg	Gln	Ser	
1105					1110					1115					1120	
Cys	Val	Ala	Leu	Val	Glu	Lys	Leu	Asn	Pro	Ile	Lys	Glu	Ser	Leu	Glu	
				1125					1130					1135		
Ala	Lys	Ser	Asn	Thr	Val	Glu	Trp	Ser	Ala	Leu	Ile	Ala	Gln	Ala	Ser	
			1140					1145					1150			
Met	Ala	Ser	Val	Asn	Leu	Ser	Ala	Gln	Pro	Tyr	Trp	Thr	Pro	Asp	Pro	
		1155					1160					1165				
Ser	Phe	Lys	Ser	Tyr	Leu	Asn	Tyr	Gly	Ala	Gly	Thr	Ser	Glu	Val	Glu	
1170						1175					1180					
Val	Asp	Ile	Leu	Thr	Gly	Ala	Thr	Thr	Ile	Leu	Arg	Ser	Asp	Leu	Val	
1185					1190					1195					1200	
Tyr	Asp	Cys	Gly	Gln	Ser	Leu	Asn	Pro	Ala	Val	Asp	Leu	Gly	Gln	Ile	
				1205					1210					1215		
Glu	Gly	Cys	Phe	Val	Gln	Gly	Ile	Gly	Phe	Phe	Thr	Asn	Glu	Asp	Tyr	
			1220					1225					1230			
Lys	Thr	Asn	Ser	Asp	Gly	Leu	Val	Ile	His	Asp	Gly	Thr	Trp	Thr	Tyr	
		1235					1240					1245				
Lys	Ile	Pro	Thr	Val	Asp	Asn	Ile	Pro	Lys	Glu	Phe	Asn	Val	Glu	Met	
		1250				1255					1260					
Phe	Asn	Ser	Ala	Pro	Asp	Lys	Lys	Arg	Val	Leu	Ser	Ser	Lys	Ala	Ser	
1265					1270					1275					1280	
Gly	Glu	Pro	Pro	Leu	Val	Leu	Ala	Thr	Ser	Val	His	Cys	Ala	Met	Arg	
				1285				1290						1295		
Glu	Ala	Ile	Arg	Ala	Ala	Arg	Lys	Glu	Phe	Ser	Val	Ser	Thr	Ser	Pro	
			1300					1305					1310			

-Ala Lys Ser Ala Val Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro
 1315 1320 1325
 Val Val Lys Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu
 1330 1335 1340
 Asn Val Ser Ala Ala Ser Ala Gly Pro Asn Thr Ala Lys Ala
 1345 1350 1355

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: maize (Zea mays L.)
- (B) STRAIN: cultivar: Golden Cross Bantam 70

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 91..4137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGCTCTCT CGGTGCAGAC GTCCGGGACT AGTACGTGGA TCGGGCCGGG GGCAACTCGA	60
GTCGTCAAGA AGGCTGCTAC CTGCTAGAGG ATG GAG ATG GGG AAG GCG GCG GCG	114
Met Glu Met Gly Lys Ala Ala Ala	1360 1365
GTG GTG CTG GCG GTG AAC GGC AAG CGG TAC GAG GCC GCC GGC GTG GAC	162
Val Val Leu Ala Val Asn Gly Lys Arg Tyr Glu Ala Ala Gly Val Asp	1370 1375 1380
CCG TCG ACG ACG CTG CTG GAG TTC CTG CGC ACC CAC ACG CCC GTC AGG	210
Pro Ser Thr Thr Leu Leu Glu Phe Leu Arg Thr His Thr Pro Val Arg	1385 1390 1395
GGG CCC AAG CTC GGC TGC GGC GAA GGT GGC TGC GGT GCA TGC GTT GTG	258
Gly Pro Lys Leu Gly Cys Gly Glu Gly Gly Cys Gly Ala Cys Val Val	1400 1405 1410
CTT GTC TCG AAG TAC GAC CCA GCC ACC GAC GAG GTG ACC GAG TTC TCA	306
Leu Val Ser Lys Tyr Asp Pro Ala Thr Asp Glu Val Thr Glu Phe Ser	1415 1420 1425 1430
GCG AGC TCC TGC CTG ACG CTG CTC CAT AGC GTG GAC CGC TGC TCG GTG	354
Ala Ser Ser Cys Leu Thr Leu Leu His Ser Val Asp Arg Cys Ser Val	

1435							1440							1445							
ACC	ACC	AGC	GAG	GGC	ATT	GGC	AAC	ACC	AAG	GAT	GGC	TAC	CAC	CCT	GTG	402					
Thr	Thr	Ser	Glu	Gly	Ile	Gly	Asn	Thr	Lys	Asp	Gly	Tyr	His	Pro	Val						
			1450					1455					1460								
CAG	CAG	CGC	CTC	TCC	GGC	TTC	CAC	GCC	TCC	CAG	TGC	GGT	TTC	TGC	ACG	450					
Gln	Gln	Arg	Leu	Ser	Gly	Phe	His	Ala	Ser	Gln	Cys	Gly	Phe	Cys	Thr						
		1465					1470					1475									
CCC	GGC	ATG	TGC	ATG	TCC	ATC	TTC	TCT	GCG	CTT	GTC	AAA	GCC	GAC	AAG	498					
Pro	Gly	Met	Cys	Met	Ser	Ile	Phe	Ser	Ala	Leu	Val	Lys	Ala	Asp	Lys						
	1480					1485					1490										
GCG	GCC	AAC	CGG	CCA	GCC	CCA	CCG	GCC	GGC	TTC	TCC	AAG	CTC	ACT	TCC	546					
Ala	Ala	Asn	Arg	Pro	Ala	Pro	Pro	Ala	Gly	Phe	Ser	Lys	Leu	Thr	Ser						
1495					1500				1505						1510						
TCG	GAG	GCT	GAG	AAG	GCT	GTC	TCT	GGC	AAC	CTG	TGC	CGC	TGC	ACA	GGG	594					
Ser	Glu	Ala	Glu	Lys	Ala	Val	Ser	Gly	Asn	Leu	Cys	Arg	Cys	Thr	Gly						
			1515					1520						1525							
TAC	AGG	CCC	ATC	GTC	GAC	GCC	TGT	AAG	AGC	TTC	GCA	GCC	GAT	GTT	GAT	642					
Tyr	Arg	Pro	Ile	Val	Asp	Ala	Cys	Lys	Ser	Phe	Ala	Ala	Asp	Val	Asp						
			1530					1535					1540								
CTT	GAG	GAC	CTG	GGC	CTC	AAC	TGC	TTC	TGG	AAG	AAG	GGT	GAT	GAG	CCT	690					
Leu	Glu	Asp	Leu	Gly	Leu	Asn	Cys	Phe	Trp	Lys	Lys	Gly	Asp	Glu	Pro						
		1545					1550					1555									
GCA	GAT	GTC	AGC	AAG	CTG	CCA	GGC	TAC	AAC	AGT	GGT	GAC	GTC	TGC	ACT	738					
Ala	Asp	Val	Ser	Lys	Leu	Pro	Gly	Tyr	Asn	Ser	Gly	Asp	Val	Cys	Thr						
	1560					1565					1570										
TTC	CCT	GAC	TTT	CTC	AAA	TCT	GAG	ATG	AAG	TCC	TCA	ATT	CAG	CAG	GCT	786					
Phe	Pro	Asp	Phe	Leu	Lys	Ser	Glu	Met	Lys	Ser	Ser	Ile	Gln	Gln	Ala						
1575					1580					1585					1590						
AAC	AGC	GCT	CCA	GTT	CCT	GTT	TCT	GAC	GAC	GGC	TGG	TAC	CGT	CCT	AGG	834					
Asn	Ser	Ala	Pro	Val	Pro	Val	Ser	Asp	Asp	Gly	Trp	Tyr	Arg	Pro	Arg						
			1595					1600						1605							
AGC	ATT	GAC	GAG	CTT	CAC	AGG	TTG	TTT	CAA	TCT	AGC	TCC	TTC	GAT	GAA	882					
Ser	Ile	Asp	Glu	Leu	His	Arg	Leu	Phe	Gln	Ser	Ser	Ser	Phe	Asp	Glu						
			1610					1615					1620								
AAT	TCC	GTG	AAG	ATA	GTG	GCT	TCA	AAC	ACT	GGG	TCT	GGA	GTG	TAC	AAG	930					
Asn	Ser	Val	Lys	Ile	Val	Ala	Ser	Asn	Thr	Gly	Ser	Gly	Val	Tyr	Lys						
		1625					1630					1635									
GAT	CAG	GAC	CTT	TAT	GAC	AAG	TAC	ATT	GAC	ATC	AAA	GGA	ATC	CCA	GAG	978					
Asp	Gln	Asp	Leu	Tyr	Asp	Lys	Tyr	Ile	Asp	Ile	Lys	Gly	Ile	Pro	Glu						
	1640					1645					1650										
CTT	TCA	GTC	ATC	AAC	AGA	AAC	GAC	AAA	GGA	ATT	GAG	CTT	GGA	TCA	GTT	1026					
Leu	Ser	Val	Ile	Asn	Arg	Asn	Asp	Lys	Gly	Ile	Glu	Leu	Gly	Ser	Val						

1655	1660	1665	1670	
GTG TCC ATC TCT AAA GCT ATT GAG GTG CTG TCA GAT GGA AAT CTC GTC Val Ser Ile Ser Lys Ala Ile Glu Val Leu Ser Asp Gly Asn Leu Val 1675 1680 1685				1074
TTC AGA AAG ATT GCT GGT CAC CTG AAC AAA GTG GCT TCA CCG TTT GTT Phe Arg Lys Ile Ala Gly His Leu Asn Lys Val Ala Ser Pro Phe Val 1690 1695 1700				1122
CGG AAC ACT GCA ACC ATA GGT GGA AAC ATA GTC ATG GCA CAA AGA TTG Arg Asn Thr Ala Thr Ile Gly Gly Asn Ile Val Met Ala Gln Arg Leu 1705 1710 1715				1170
CCA TTC GCA TCG GAC ATT GCA ACC ATA CTA CTA GCT GCA GGT TCA ACA Pro Phe Ala Ser Asp Ile Ala Thr Ile Leu Leu Ala Ala Gly Ser Thr 1720 1725 1730				1218
GTC ACA ATC CAG GTG GCT TCC AAA AGG CTG TGC TTC ACT CTG GAG GAG Val Thr Ile Gln Val Ala Ser Lys Arg Leu Cys Phe Thr Leu Glu Glu 1735 1740 1745 1750				1266
TTC TTG CAG CAG CCT CCA TGC GAT TCT AGG ACC CTG CTG CTG AGC ATA Phe Leu Gln Gln Pro Pro Cys Asp Ser Arg Thr Leu Leu Leu Ser Ile 1755 1760 1765				1314
TTT ATC CCG GAA TGG GGC TCA AAT GAT GTC ACC TTT GAG ACT TTC CGA Phe Ile Pro Glu Trp Gly Ser Asn Asp Val Thr Phe Glu Thr Phe Arg 1770 1775 1780				1362
GCA GCA CCT CGT CCA CTT GGC AAT GCT GTC TCA TAT GTC AAT TCA GCT Ala Ala Pro Arg Pro Leu Gly Asn Ala Val Ser Tyr Val Asn Ser Ala 1785 1790 1795				1410
TTC TTG GCA AGG ACT TCA TTG GAT GCA GCA TCA AAG GAC CAT CTC ATC Phe Leu Ala Arg Thr Ser Leu Asp Ala Ala Ser Lys Asp His Leu Ile 1800 1805 1810				1458
GAG GAT ATA TGT CTG GCG TTC GGT GCT TAT GGA GCT GAT CAT GCT ATT Glu Asp Ile Cys Leu Ala Phe Gly Ala Tyr Gly Ala Asp His Ala Ile 1815 1820 1825 1830				1506
AGA GCT AGA AAG GTT GAG GAT TAC CTG AAG GGC AAA ACA GTG AGC TCG Arg Ala Arg Lys Val Glu Asp Tyr Leu Lys Gly Lys Thr Val Ser Ser 1835 1840 1845				1554
TCT GTC ATA CTT GAA GCT GTT CGG TTG CTT AAA GGG TCT ATT AAA CCA Ser Val Ile Leu Glu Ala Val Arg Leu Leu Lys Gly Ser Ile Lys Pro 1850 1855 1860				1602
TCA GAA GGC TCA ACA CAT CCT GAG TAT AGA ATT AGC TTG GCT GTC AGT Ser Glu Gly Ser Thr His Pro Glu Tyr Arg Ile Ser Leu Ala Val Ser 1865 1870 1875				1650
TTC TTG TTT ACC TTC CTA TCC TCC CTT GCC AAC AGC TTG AAT GAA TCT Phe Leu Phe Thr Phe Leu Ser Ser Leu Ala Asn Ser Leu Asn Glu Ser				1698

1880	1885	1890	
GCA AAG GTT AGT GGT ACC AAC GAG CAC TCA CCA GAG AAG CAA CTC AAG Ala Lys Val Ser Gly Thr Asn Glu His Ser Pro Glu Lys Gln Leu Lys 1895 1900 1905 1910			1746
TTG GAC ATC AAT GAT TTG CCA ATA CGA TCA AGA CAA GAA ATA TTT TTC Leu Asp Ile Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Ile Phe Phe 1915 1920 1925			1794
ACT GAT GCA TAT AAG CCA GTT GGC AAA GCA ATT AAG AAA GCT GGG GTA Thr Asp Ala Tyr Lys Pro Val Gly Lys Ala Ile Lys Lys Ala Gly Val 1930 1935 1940			1842
GAG ATC CAA GCT TCA GGG GAA GCT GTG TAC GTT GAT GAT ATC CCT GCT Glu Ile Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro Ala 1945 1950 1955			1890
CCC AAA GAT TGC CTC TAT GGG GCA TTT ATT TAT AGC ACA CAC CCT CAT Pro Lys Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro His 1960 1965 1970			1938
GCA CAT GTA AAG TCA ATC AAC TTT AAA CCA TCT TTG GCT TCA CAG AAG Ala His Val Lys Ser Ile Asn Phe Lys Pro Ser Leu Ala Ser Gln Lys 1975 1980 1985 1990			1986
ATC ATC ACA GTT ATC ACT GCA AAG GAT ATT CCC AGC GGT GGA CAA AAT Ile Ile Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Gln Asn 1995 2000 2005			2034
GTT GGT TAT AGC TTC CCG ATG ATT GGA GAA GAA GCA CTT TTT GCA GAT Val Gly Tyr Ser Phe Pro Met Ile Gly Glu Glu Ala Leu Phe Ala Asp 2010 2015 2020			2082
CCA GTT GCT GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT CAA Pro Val Ala Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Gln 2025 2030 2035			2130
ACA CAG AAG TAT GCC TAC ATG GCG GCA AAG CAA GCC ATC ATT GAG TAT Thr Gln Lys Tyr Ala Tyr Met Ala Ala Lys Gln Ala Ile Ile Glu Tyr 2040 2045 2050			2178
AGC ACA GAA AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCA ATT Ser Thr Glu Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile 2055 2060 2065 2070			2226
GAA CGA AGC AGC TTC TTC CAA ACC CTC CCA TTT GTA GCT CCT AAG CCA Glu Arg Ser Ser Phe Phe Gln Thr Leu Pro Phe Val Ala Pro Lys Pro 2075 2080 2085			2274
GTT GGT GAT TAC GAC AAA GGG ATG TCT GAA GCT GAT CAC AAG ATT TTA Val Gly Asp Tyr Asp Lys Gly Met Ser Glu Ala Asp His Lys Ile Leu 2090 2095 2100			2322
TCG GCA GAG GTA AAA ATT GAA TCC CAA TAC TTT TTC TAC ATG GAG CCA Ser Ala Glu Val Lys Ile Glu Ser Gln Tyr Phe Phe Tyr Met Glu Pro 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000			2370

2105	2110	2115	
CAA GTG GCG CTA GCT ATT CCT GAT GAA GAT AAC TGC ATA ACC ATC TAT Gln Val Ala Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr 2120 2125 2130			2418
TTT TCG ACA CAA TTA CCT GAG TCC ACA CAA AAT GTG GTT GCA AAG TGC Phe Ser Thr Gln Leu Pro Glu Ser Thr Gln Asn Val Val Ala Lys Cys 2135 2140 2145 2150			2466
GTT GGC ATT CCA TTT CAC AAT GTC CGT GTA ATC ACC AGA AGG GTC GGA Val Gly Ile Pro Phe His Asn Val Arg Val Ile Thr Arg Arg Val Gly 2155 2160 2165			2514
GGA GGC TTT GGT GGA AAA GCA TTG AAA TCA ATG CAT GTT GCA TGT GCA Gly Gly Phe Gly Gly Lys Ala Leu Lys Ser Met His Val Ala Cys Ala 2170 2175 2180			2562
TGT GCA GTT GCT GCA TTG AAG CTA CAA CGT CCA GTT CGG ATG TAC CTC Cys Ala Val Ala Ala Leu Lys Leu Gln Arg Pro Val Arg Met Tyr Leu 2185 2190 2195			2610
GAT CGC AAG ACA GAC ATG ATA ATG GCA GGC GGG CGG CAT CCT ATG AAG Asp Arg Lys Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys 2200 2205 2210			2658
GTG AAG TAC TCT GTT GGG TTC AAG TCA AAC GGC AAG ATC ACA GCC TTA Val Lys Tyr Ser Val Gly Phe Lys Ser Asn Gly Lys Ile Thr Ala Leu 2215 2220 2225 2230			2706
CAT CTT GAT CTT GGG ATC AAT GGT GGA ATA TCT CCA GAT ATG AGT CCA His Leu Asp Leu Gly Ile Asn Gly Gly Ile Ser Pro Asp Met Ser Pro 2235 2240 2245			2754
ATG ATT GCA GCA CCT GTC ATA GGT TCT CTC AAA AAG TAC AAC TGG GGC Met Ile Ala Ala Pro Val Ile Gly Ser Leu Lys Lys Tyr Asn Trp Gly 2250 2255 2260			2802
AAT CTT GCA TTT GAC ACC AAG GTC TGC AAA ACA AAT GTC TCA TCA AAA Asn Leu Ala Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys 2265 2270 2275			2850
TCG TCA ATG AGA GCT CCT GGA GAT GCG CAG GGC TCT TTC ATT GCT GAA Ser Ser Met Arg Ala Pro Gly Asp Ala Gln Gly Ser Phe Ile Ala Glu 2280 2285 2290			2898
GCC ATC ATC GAG CAT GTT GCC TCG GCA CTT TCA GCC GAC ACT AAT ACC Ala Ile Ile Glu His Val Ala Ser Ala Leu Ser Ala Asp Thr Asn Thr 2295 2300 2305 2310			2946
ATA AGG AGA AAG AAC CTT CAT GAC TTT GAG AGC CTT GCA GTG TTC TTT Ile Arg Arg Lys Asn Leu His Asp Phe Glu Ser Leu Ala Val Phe Phe 2315 2320 2325			2994
GGA GAT AGT GCA GGT GAA GCT TCT ACA TAC AGC CTT GTC ACC ATG TTC Gly Asp Ser Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Thr Met Phe 3042			

2330						2335						2340						
GAT Asp	AAA Lys	TTG Leu	GCC Ala	TCC Ser	TCT Ser	CCA Pro	GAA Glu	TAC Tyr	CAG Gln	CAC His	CGA Arg	GCT Ala	GAA Glu	ATG Met	GTG Val	3090		
		2345				2350						2355						
GAA Glu	CAA Gln	TTC Phe	AAC Asn	CGA Arg	AGC Ser	AAC Asn	AAG Lys	TGG Trp	AAG Lys	AAG Lys	CGT Arg	GGC Gly	ATT Ile	TCT Ser	TGT Cys	3138		
		2360				2365						2370						
GTG Val	CCT Pro	GTA Val	ACA Thr	TAT Tyr	GAG Glu	GTG Val	CAG Gln	CTT Leu	CGG Arg	CCA Pro	ACT Thr	CCA Pro	GGA Gly	AAG Lys	GTG Val	3186		
				2380						2385						2390		
TCT Ser	ATC Ile	ATG Met	AAT Asn	GAT Asp	GGT Gly	TCC Ser	ATT Ile	GCT Ala	GTT Val	GAG Glu	GTT Val	GGA Gly	GGG Gly	GTT Val	GAG Glu	3234		
				2395				2400						2405				
CTA Leu	GGC Gly	CAA Gln	GGG Gly	TTG Leu	TGG Trp	ACA Thr	AAA Lys	GTG Val	AAG Lys	CAG Gln	ATG Met	ACG Thr	GCA Ala	TTC Phe	GGA Gly	3282		
				2410				2415						2420				
CTA Leu	GGA Gly	CAG Gln	CTG Leu	TGT Cys	CCT Pro	GGC Gly	GGC Gly	GGT Gly	GAA Glu	AGC Ser	CTT Leu	CTA Leu	GAC Asp	AAG Lys	GTG Val	3330		
		2425				2430						2435						
CGG Arg	GTC Val	ATC Ile	CAG Gln	GCC Ala	GAC Asp	ACA Thr	TTG Leu	AGC Ser	ATG Met	ATC Ile	CAA Gln	GGA Gly	GGG Gly	GTC Val	ACT Thr	3378		
		2440				2445						2450						
GGT Gly	GGG Gly	AGC Ser	ACC Thr	ACT Thr	TCT Ser	GAA Glu	ACT Thr	AGC Ser	TGT Cys	GAA Glu	GCA Ala	GTT Val	CGT Arg	AAG Lys	TCG Ser	3426		
2455				2460						2465						2470		
TGT Cys	GTT Val	GCA Ala	CTC Leu	GTC Val	GAG Glu	AGC Ser	TTG Leu	AAG Lys	CCA Pro	ATC Ile	AAG Lys	GAG Glu	AAT Asn	CTG Leu	GAG Glu	3474		
				2475				2480						2485				
GCT Ala	AAA Lys	ACT Thr	GGC Gly	ACA Thr	GTG Val	GAA Glu	TGG Trp	AGT Ser	GCC Ala	TTG Leu	ATT Ile	GCA Ala	CAG Gln	GCA Ala	AGT Ser	3522		
		2490						2495				2500						
ATG Met	GCG Ala	AGC Ser	GTT Val	AAC Asn	TTA Leu	TCG Ser	GCA Ala	CAT His	GCA Ala	TAC Tyr	TGG Trp	ACC Thr	CCT Pro	GAT Asp	CCA Pro	3570		
		2505				2510						2515						
ACT Thr	TTC Phe	ACA Thr	AGC Ser	TAT Tyr	TTG Leu	AAC Asn	TAC Tyr	GGA Gly	GCC Ala	GGC Gly	ACT Thr	AGC Ser	GAG Glu	GTG Val	GAA Glu	3618		
		2520				2525				2530								
ATT Ile	GAT Asp	GTC Val	CTG Leu	ACA Thr	GGA Gly	GCA Ala	ACA Thr	ACA Thr	ATT Ile	CTA Leu	AGG Arg	AGT Ser	GAC Asp	CTT Leu	GTC Val	3666		
2535				2540						2545						2550		
TAC Tyr	GAT Asp	TGC Cys	GGG Gly	CAA Gln	AGC Ser	TTG Leu	AAC Asn	CCT Pro	GCT Ala	GTC Val	GAT Asp	TTG Leu	GGG Gly	CAG Gln	GTG Val	3714		

2555	2560	2565	
GAA GGT GCA TTC GTA CAA GGA GTA GGC TTC TTC ACA AAC GAG GAG TAC Glu Gly Ala Phe Val Gln Gly Val Gly Phe Phe Thr Asn Glu Glu Tyr 2570 2575 2580			3762
GCA ACC AAC TCT GAC GGG TTG GTC ATC CAC GAT GGC ACA TGG ACG TAC Ala Thr Asn Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr 2585 2590 2595			3810
AAG ATC CCC ACG GTC GAC ACC ATC CCA AAG CAG TTC AAC GTT GAG CTG Lys Ile Pro Thr Val Asp Thr Ile Pro Lys Gln Phe Asn Val Glu Leu 2600 2605 2610			3858
ATC AAC AGC GCC CGT GAC CAG AAG CGC GTC CTC TCT TCC AAA GCA TCG Ile Asn Ser Ala Arg Asp Gln Lys Arg Val Leu Ser Ser Lys Ala Ser 2615 2620 2625 2630			3906
GGC GAG CCT CCG CTT CTC CTA GCT TCC TCT GTG CAC TGC GCA ATG AGG Gly Glu Pro Pro Leu Leu Leu Ala Ser Ser Val His Cys Ala Met Arg 2635 2640 2645			3954
GAG GCC ATC AGG GCC GCC AGG AAA GAA TTC TCG GTC TGC ACT GGT CCA Glu Ala Ile Arg Ala Ala Arg Lys Glu Phe Ser Val Cys Thr Gly Pro 2650 2655 2660			4002
GCG AAC TCC GCC ATC ACG TTC CAG ATG GAC GTG CCG GCA ACG ATG CCT Ala Asn Ser Ala Ile Thr Phe Gln Met Asp Val Pro Ala Thr Met Pro 2665 2670 2675			4050
GTC GTC AAG GAG CTC TGC GGC CTG GAT GTC GTT GAG AGG TAC CTG GAG Val Val Lys Glu Leu Cys Gly Leu Asp Val Val Glu Arg Tyr Leu Glu 2680 2685 2690			4098
AGC GTG TCG GCT GCC AGC CCA ACA AAC ACC GCT AAA GCA TAGATCCAGT Ser Val Ser Ala Ala Ser Pro Thr Asn Thr Ala Lys Ala 2695 2700 2705			4147
AGGCGCTCTA TCCATGGTGT GATGGCTTAA TCAATCTGTA AAACACTAAG CGGCGTGACA			4207
TGCCGAGCTT TCAGTGTTAG CTATGATGTA CAGAAGAAGA GGTACCAATG GCGAGTTGTG			4267
GCCATGCGAA TCAGGAGTCA TGAACCATTG AGGGGGGAAA TAAAGTAAAT AAGTGTTGCG			4327
CCGGCGAAAA AAAAAAAAAA AAAAAAAAAA AA			4359

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Met	Gly	Lys	Ala	Ala	Ala	Val	Val	Leu	Ala	Val	Asn	Gly	Lys	1	5	10	15
Arg	Tyr	Glu	Ala	Ala	Gly	Val	Asp	Pro	Ser	Thr	Thr	Leu	Leu	Glu	Phe	20	25	30	
Leu	Arg	Thr	His	Thr	Pro	Val	Arg	Gly	Pro	Lys	Leu	Gly	Cys	Gly	Glu	35	40	45	
Gly	Gly	Cys	Gly	Ala	Cys	Val	Val	Leu	Val	Ser	Lys	Tyr	Asp	Pro	Ala	50	55	60	
Thr	Asp	Glu	Val	Thr	Glu	Phe	Ser	Ala	Ser	Ser	Cys	Leu	Thr	Leu	Leu	65	70	75	80
His	Ser	Val	Asp	Arg	Cys	Ser	Val	Thr	Thr	Ser	Glu	Gly	Ile	Gly	Asn	85	90	95	
Thr	Lys	Asp	Gly	Tyr	His	Pro	Val	Gln	Gln	Arg	Leu	Ser	Gly	Phe	His	100	105	110	
Ala	Ser	Gln	Cys	Gly	Phe	Cys	Thr	Pro	Gly	Met	Cys	Met	Ser	Ile	Phe	115	120	125	
Ser	Ala	Leu	Val	Lys	Ala	Asp	Lys	Ala	Ala	Asn	Arg	Pro	Ala	Pro	Pro	130	135	140	
Ala	Gly	Phe	Ser	Lys	Leu	Thr	Ser	Ser	Glu	Ala	Glu	Lys	Ala	Val	Ser	145	150	155	160
Gly	Asn	Leu	Cys	Arg	Cys	Thr	Gly	Tyr	Arg	Pro	Ile	Val	Asp	Ala	Cys	165	170	175	
Lys	Ser	Phe	Ala	Ala	Asp	Val	Asp	Leu	Glu	Asp	Leu	Gly	Leu	Asn	Cys	180	185	190	
Phe	Trp	Lys	Lys	Gly	Asp	Glu	Pro	Ala	Asp	Val	Ser	Lys	Leu	Pro	Gly	195	200	205	
Tyr	Asn	Ser	Gly	Asp	Val	Cys	Thr	Phe	Pro	Asp	Phe	Leu	Lys	Ser	Glu	210	215	220	
Met	Lys	Ser	Ser	Ile	Gln	Gln	Ala	Asn	Ser	Ala	Pro	Val	Pro	Val	Ser	225	230	235	240
Asp	Asp	Gly	Trp	Tyr	Arg	Pro	Arg	Ser	Ile	Asp	Glu	Leu	His	Arg	Leu	245	250	255	
Phe	Gln	Ser	Ser	Ser	Phe	Asp	Glu	Asn	Ser	Val	Lys	Ile	Val	Ala	Ser	260	265	270	
Asn	Thr	Gly	Ser	Gly	Val	Tyr	Lys	Asp	Gln	Asp	Leu	Tyr	Asp	Lys	Tyr	275	280	285	

Ile	Asp	Ile	Lys	Gly	Ile	Pro	Glu	Leu	Ser	Val	Ile	Asn	Arg	Asn	Asp	290	295	300
Lys	Gly	Ile	Glu	Leu	Gly	Ser	Val	Val	Ser	Ile	Ser	Lys	Ala	Ile	Glu	305	310	315
Val	Leu	Ser	Asp	Gly	Asn	Leu	Val	Phe	Arg	Lys	Ile	Ala	Gly	His	Leu	325	330	335
Asn	Lys	Val	Ala	Ser	Pro	Phe	Val	Arg	Asn	Thr	Ala	Thr	Ile	Gly	Gly	340	345	350
Asn	Ile	Val	Met	Ala	Gln	Arg	Leu	Pro	Phe	Ala	Ser	Asp	Ile	Ala	Thr	355	360	365
Ile	Leu	Leu	Ala	Ala	Gly	Ser	Thr	Val	Thr	Ile	Gln	Val	Ala	Ser	Lys	370	375	380
Arg	Leu	Cys	Phe	Thr	Leu	Glu	Glu	Phe	Leu	Gln	Gln	Pro	Pro	Cys	Asp	385	390	395
Ser	Arg	Thr	Leu	Leu	Leu	Ser	Ile	Phe	Ile	Pro	Glu	Trp	Gly	Ser	Asn	405	410	415
Asp	Val	Thr	Phe	Glu	Thr	Phe	Arg	Ala	Ala	Pro	Arg	Pro	Leu	Gly	Asn	420	425	430
Ala	Val	Ser	Tyr	Val	Asn	Ser	Ala	Phe	Leu	Ala	Arg	Thr	Ser	Leu	Asp	435	440	445
Ala	Ala	Ser	Lys	Asp	His	Leu	Ile	Glu	Asp	Ile	Cys	Leu	Ala	Phe	Gly	450	455	460
Ala	Tyr	Gly	Ala	Asp	His	Ala	Ile	Arg	Ala	Arg	Lys	Val	Glu	Asp	Tyr	465	470	475
Leu	Lys	Gly	Lys	Thr	Val	Ser	Ser	Ser	Val	Ile	Leu	Glu	Ala	Val	Arg	485	490	495
Leu	Leu	Lys	Gly	Ser	Ile	Lys	Pro	Ser	Glu	Gly	Ser	Thr	His	Pro	Glu	500	505	510
Tyr	Arg	Ile	Ser	Leu	Ala	Val	Ser	Phe	Leu	Phe	Thr	Phe	Leu	Ser	Ser	515	520	525
Leu	Ala	Asn	Ser	Leu	Asn	Glu	Ser	Ala	Lys	Val	Ser	Gly	Thr	Asn	Glu	530	535	540
His	Ser	Pro	Glu	Lys	Gln	Leu	Lys	Leu	Asp	Ile	Asn	Asp	Leu	Pro	Ile	545	550	555
Arg	Ser	Arg	Gln	Glu	Ile	Phe	Phe	Thr	Asp	Ala	Tyr	Lys	Pro	Val	Gly	565	570	575
Lys	Ala	Ile	Lys	Lys	Ala	Gly	Val	Glu	Ile	Gln	Ala	Ser	Gly	Glu	Ala	580	585	590

- Val	Tyr	Val	Asp	Asp	Ile	Pro	Ala	Pro	Lys	Asp	Cys	Leu	Tyr	Gly	Ala		
		595					600					605					
Phe	Ile	Tyr	Ser	Thr	His	Pro	His	Ala	His	Val	Lys	Ser	Ile	Asn	Phe		
	610					615					620						
Lys	Pro	Ser	Leu	Ala	Ser	Gln	Lys	Ile	Ile	Thr	Val	Ile	Thr	Ala	Lys		
	625				630					635					640		
Asp	Ile	Pro	Ser	Gly	Gly	Gln	Asn	Val	Gly	Tyr	Ser	Phe	Pro	Met	Ile		
				645					650					655			
Gly	Glu	Glu	Ala	Leu	Phe	Ala	Asp	Pro	Val	Ala	Glu	Phe	Ala	Gly	Gln		
			660					665					670				
Asn	Ile	Gly	Val	Val	Ile	Ala	Gln	Thr	Gln	Lys	Tyr	Ala	Tyr	Met	Ala		
		675					680					685					
Ala	Lys	Gln	Ala	Ile	Ile	Glu	Tyr	Ser	Thr	Glu	Asn	Leu	Gln	Pro	Pro		
	690					695					700						
Ile	Leu	Thr	Ile	Glu	Asp	Ala	Ile	Glu	Arg	Ser	Ser	Phe	Phe	Gln	Thr		
	705				710					715					720		
Leu	Pro	Phe	Val	Ala	Pro	Lys	Pro	Val	Gly	Asp	Tyr	Asp	Lys	Gly	Met		
			725						730					735			
Ser	Glu	Ala	Asp	His	Lys	Ile	Leu	Ser	Ala	Glu	Val	Lys	Ile	Glu	Ser		
			740					745					750				
Gln	Tyr	Phe	Phe	Tyr	Met	Glu	Pro	Gln	Val	Ala	Leu	Ala	Ile	Pro	Asp		
		755					760					765					
Glu	Asp	Asn	Cys	Ile	Thr	Ile	Tyr	Phe	Ser	Thr	Gln	Leu	Pro	Glu	Ser		
	770					775					780						
Thr	Gln	Asn	Val	Val	Ala	Lys	Cys	Val	Gly	Ile	Pro	Phe	His	Asn	Val		
	785				790					795					800		
Arg	Val	Ile	Thr	Arg	Arg	Val	Gly	Gly	Gly	Phe	Gly	Gly	Lys	Ala	Leu		
				805				810						815			
Lys	Ser	Met	His	Val	Ala	Cys	Ala	Cys	Ala	Val	Ala	Ala	Leu	Lys	Leu		
			820					825					830				
Gln	Arg	Pro	Val	Arg	Met	Tyr	Leu	Asp	Arg	Lys	Thr	Asp	Met	Ile	Met		
		835					840					845					
Ala	Gly	Gly	Arg	His	Pro	Met	Lys	Val	Lys	Tyr	Ser	Val	Gly	Phe	Lys		
	850					855					860						
Ser	Asn	Gly	Lys	Ile	Thr	Ala	Leu	His	Leu	Asp	Leu	Gly	Ile	Asn	Gly		
	865				870					875					880		
Gly	Ile	Ser	Pro	Asp	Met	Ser	Pro	Met	Ile	Ala	Ala	Pro	Val	Ile	Gly		
				885					890					895			

-Ser Leu Lys Lys Tyr Asn Trp Gly Asn Leu Ala Phe Asp Thr Lys Val
 900 905 910
 Cys Lys Thr Asn Val Ser Ser Lys Ser Ser Met Arg Ala Pro Gly Asp
 915 920 925
 Ala Gln Gly Ser Phe Ile Ala Glu Ala Ile Ile Glu His Val Ala Ser
 930 935 940
 Ala Leu Ser Ala Asp Thr Asn Thr Ile Arg Arg Lys Asn Leu His Asp
 945 950 955 960
 Phe Glu Ser Leu Ala Val Phe Phe Gly Asp Ser Ala Gly Glu Ala Ser
 965 970 975
 Thr Tyr Ser Leu Val Thr Met Phe Asp Lys Leu Ala Ser Ser Pro Glu
 980 985 990
 Tyr Gln His Arg Ala Glu Met Val Glu Gln Phe Asn Arg Ser Asn Lys
 995 1000 1005
 Trp Lys Lys Arg Gly Ile Ser Cys Val Pro Val Thr Tyr Glu Val Gln
 1010 1015 1020
 Leu Arg Pro Thr Pro Gly Lys Val Ser Ile Met Asn Asp Gly Ser Ile
 1025 1030 1035 1040
 Ala Val Glu Val Gly Gly Val Glu Leu Gly Gln Gly Leu Trp Thr Lys
 1045 1050 1055
 Val Lys Gln Met Thr Ala Phe Gly Leu Gly Gln Leu Cys Pro Gly Gly
 1060 1065 1070
 Gly Glu Ser Leu Leu Asp Lys Val Arg Val Ile Gln Ala Asp Thr Leu
 1075 1080 1085
 Ser Met Ile Gln Gly Gly Val Thr Gly Gly Ser Thr Thr Ser Glu Thr
 1090 1095 1100
 Ser Cys Glu Ala Val Arg Lys Ser Cys Val Ala Leu Val Glu Ser Leu
 1105 1110 1115 1120
 Lys Pro Ile Lys Glu Asn Leu Glu Ala Lys Thr Gly Thr Val Glu Trp
 1125 1130 1135
 Ser Ala Leu Ile Ala Gln Ala Ser Met Ala Ser Val Asn Leu Ser Ala
 1140 1145 1150
 His Ala Tyr Trp Thr Pro Asp Pro Thr Phe Thr Ser Tyr Leu Asn Tyr
 1155 1160 1165
 Gly Ala Gly Thr Ser Glu Val Glu Ile Asp Val Leu Thr Gly Ala Thr
 1170 1175 1180
 Thr Ile Leu Arg Ser Asp Leu Val Tyr Asp Cys Gly Gln Ser Leu Asn
 1185 1190 1195 1200

-Pro Ala Val Asp Leu Gly Gln Val Glu Gly Ala Phe Val Gln Gly Val
 1205 1210 1215
 Gly Phe Phe Thr Asn Glu Glu Tyr Ala Thr Asn Ser Asp Gly Leu Val
 1220 1225 1230
 Ile His Asp Gly Thr Trp Thr Tyr Lys Ile Pro Thr Val Asp Thr Ile
 1235 1240 1245
 Pro Lys Gln Phe Asn Val Glu Leu Ile Asn Ser Ala Arg Asp Gln Lys
 1250 1255 1260
 Arg Val Leu Ser Ser Lys Ala Ser Gly Glu Pro Pro Leu Leu Leu Ala
 1265 1270 1275 1280
 Ser Ser Val His Cys Ala Met Arg Glu Ala Ile Arg Ala Ala Arg Lys
 1285 1290 1295
 Glu Phe Ser Val Cys Thr Gly Pro Ala Asn Ser Ala Ile Thr Phe Gln
 1300 1305 1310
 Met Asp Val Pro Ala Thr Met Pro Val Val Lys Glu Leu Cys Gly Leu
 1315 1320 1325
 Asp Val Val Glu Arg Tyr Leu Glu Ser Val Ser Ala Ala Ser Pro Thr
 1330 1335 1340
 Asn Thr Ala Lys Ala
 1345

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide primer
(23-mer in anti-sense orientation)"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 21

(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCANGTNC CRTCTTGNAT NAC

23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(23-mer in sense orientation)"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 3

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 9

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 12

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 18

(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGNGARGCNG TNTAYGTNGA YGA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGGTCAAA ATATTGGTGT CGTGATTG

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATTGCTGAA ACACAAAGAT ATGCTAAT

28

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGCTGCAGA TTTTCTGTGC TATACTC

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCTTTGCAG CCATATTAGC ATATCTT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACAGCCTTTT GGAAGCCACC TGGA

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATCGGACTTG TTGTCGGCCT TGAC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer
(sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTGCTCAA ACACAGAAGT ATGCCTAC

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTTGCCGCC ATGTAGGCAT ACTTC

25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide primer
(anti-sense) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCCACCTAT GGTTGCAGTG TTCC

24